Remarks

Applicants acknowledge the Examiner's withdrawal of Claims 4-10 and 14-19. Claims 2-10 and 14-19 have been cancelled. Applicants, of course, reserve the right to file one or more divisional applications directed to the subject matter contained within the cancelled Claims.

In accordance with the Examiner's helpful suggestion, the Applicants have amended Claims 11-13, so that they no longer refer to non-elected subject matter.

In further accord with the Examiner's helpful suggestion, the Applicants have amended the Specification to revise minor informalities. Specifically, the Applicants have added sequence identifiers to Figure 1, which correspond to the sequence listing submitted by the Applicant. Further, Applicant has deleted reference to Genbank accession numbers and identified the full chemical indicator for "POPS." As a result of these amendments to the Specification and Figure 1, no new matter has been added.

Claims 1-3 have been rejected under 35 U.S.C. §101. In view of the Examiner's helpful comments, the Applicants have amended Claim 1 to clearly point out that SEQ ID No: 2 is an isolated and purified protein. As a result, Applicants respectfully submit that the rejection under 35 U.S.C. §101 is now obviated.

Claim Rejections Under 35 U.S.C. §112

Claims 1, 3, and 11-13 have been rejected under 35 U.S.C. §112, 1st paragraph. Applicants respectfully submit that as a result of the amendments to Claim 1 and 11-13, the rejection is now obviated. Specifically, the Applicants have directed Claim 1 to "a human group

IIF secreted phospholipase ($sPLA_2$)," which consists essentially of SEQ ID No: 2. As a result, the Applicants' Claims are no longer directed to "all mammalian secreted group IIF $sPLA_2$." Further, Applicants respectfully submit that the inclusion of a SEQ ID No clearly identifies a structural characteristic of the protein, and hence Claim 1 and dependent claims thereof are fully enabled as they clearly have a predictable structure. Further, Applicants have amended Claims 12 and 13 to recite that the pharmaceutical composition according to Claim 11 is **suitable** to treat both viral and bacterial infections, as well as cancers. Consequently, Applicants' Claims 11-13 show a polypeptide pharmaceutical composition, which has demonstrated specific enzymatic and catalytic activity, wherein said composition is capable of treating viral and bacterial infections, and cancer.

One skilled in the art would readily recognize the Applicants' polypeptide and formulating a pharmaceutical composition from that peptide. Subsequent testing of the pharmaceutical composition containing the polypeptide of SEQ ID No: 2 to determine its catalytic roles on various viral and bacterial infections and cancers, is well within the abilities of one skilled in the art.

Claims 1-3 and 11-13 have been rejected under 35 U.S.C. §112, 2nd paragraph. Applicants respectfully submit that as a result of the Claim amendments, this objection is now obviated. The Applicant has clarified the acronym "$sPLA_2$" and deleted reference to "hydrolyzes phosphatidylglycerol versus phosphatidylcholine with about a 15-fold preference." As a result, Applicants respectfully submit the rejections under §112, 2nd paragraph are now obviated.

Claim Rejections Under 35 U.S.C. §102(a)

Claim 1, 3 and 11-13 have been rejected under 35 U.S.C. §102(a) as being anticipated by Valentine et al. Applicants respectfully submit that as a result of the amendment to incorporate SEQ ID No. 2 into Claim 1, the rejection under Valentine et al. is now obviated. Specifically, Claim 1 now refers to SEQ ID No: 2, which consists essentially of a 169 amino acid polypeptide. Nowhere in Valentine et al., is there a teaching or suggestion of such a polypeptide.

Claims 1-3, and 11-13 have been rejected under 35 U.S.C. §102(e) as being anticipated by Das et al. Applicants respectfully submit that as a result of the amendment to Claim 1, the rejection under Das et al. is now obviated. Specifically, the Applicants SEQ ID No: 2 has a 43 amino acids N-terminal deletion when compared to the sequence disclosed in Das et al. As a result, Das et al. teach a polypeptide having 43 additional amino acid residues at the N-terminal chain of the polypeptide, as compared to the SEQ ID No: 2 of the Applicants' invention. Clearly, one skilled in the art would recognize that these additional 43 residues affect both the structure and function of the Das et al. polypeptide. As is well known in the art, the interaction between amino acid residues at the end of an alpha-helix segment and an electric dipole inherent to the alpha-helices clearly affect the folding and segmentation of a polypeptide chain, and thus the activity and structure. Nowhere in Das et al. is there a suggestion that of deleting these 43 amino acid residues has no subsequent affect on the polypeptide stability and/or function. Furthermore, one skilled in the art would recognize that Proline is unique among the twenty genetically encoded amino acids in that it does not have an NH-C-CO- backbone. Hence, its backbone is more rigid, making it the most tightly constrained of all amino acids in terms of the

configurations it can assume. Applicants respectfully submit that a study of the extra 43 residues in the sequence shown by Das et al. reveals 3 Proline residues, which inherently rigidify the polypeptide of Das et al. As a result, the Applicants respectfully submit that these additional 43 amino acids of the Das et al. sequence fail to anticipate the Applicants' SEQ ID No: 2.

We invite the examiner's attention to the case of In re Deule, 34 USPQ2d 1210 (Fed. Cir. 1995), where the court held that the rejection of claims drawn to a particular DNA sequence was improper when the reference used in the prior rejection failed to teach the DNA molecules. Applicants respectfully submit that the facts of In re Deule are analogous to the facts of this case. The court In re Deule noted that:

> "While the general idea of the claimed molecules, their function, and their general chemical nature may have been obvious under Bohlen's teachings, and the knowledge that some genes existed may have been clear, the precise cDNA molecules of Claims 5 and 7 would not have been obvious over the Bohlen reference because Bohlen teaches proteins, not the claimed or closely related cDNA molecules. The redundancy of the genetic code precluded contemplation of or focus on the specific cDNA molecules of Claims 5 and 7... Similarly, knowledge of a protein does not give one a conception of a particular DNA encoding it. Thus, a fortiori, Bohlen's disclosure of the N-terminal portion of a protein, which the PTO urges is the same as HBGF, would not have suggested the particular cDNA molecules defined by Claims 5 and 7. This is so even though one skilled in the art knew that some DNA, albeit not in purified and isolated form, did exist. The compounds of Claims 5 and 7 are specific compounds not suggested by the prior art.

Similar to the case of In re Deule, the current application describes a different sequence than that disclosed in Das et al.

In view of the foregoing, Applicants respectfully submit the Application is now in a condition for allowance, which action is respectfully requested.

Respectfully submitted,

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